SEQUENCE LISTING

<110> UEMURA, Hidetoshi
OKUI, Akira
KOMINAMI, Katsuya
YAMAGUCHI, Nozomi
MITSUI, Shinichi

<120> NOVEL SERINE PROTEASE BSSP6

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<140> 09/856,320
<141> 2001-05-21

<150> JP 10-347802
<151> 1998-11-20

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<170> PatentIn version 3.1

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Met Gln

agg ttg agg tgg ctg cgg gac tgg aag tca tcg ggc aga ggt ctc aca 166
Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly Leu Thr
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gca gcc aag gaa cct ggg gcc cgc tcc tcc ccc ctc cag gcc atg agg 214
Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met Arg
-35 -30 -25 -20

att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg gga 262
Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
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gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc 310
Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
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tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg acg 358

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Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr
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ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccc      406
Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
30                  35                  40                  45

cgc tac ata gtt cac ctg ggg cag cac aac ctc cag aag gag gag ggc      454
Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly
                50                  55                  60

tgt gag cag acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc ttc      502
Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe
            65                  70                  75

aac aac agc ctc ccc aac aaa gac cac cgc aat gac atc atg ctg gtg      550
Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val
        80                  85                  90

aag atg gca tcg cca gtc tcc atc acc tgg gct gtg cga ccc ctc acc      598
Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr
    95                  100                 105

ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc ggc      646
Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly
110                 115                 120                 125

tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg cga      694
Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg
                130                 135                 140

tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc tac      742
Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr
            145                 150                 155

ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa ggg      790
Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly
        160                 165                 170

ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt aac      838
Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
    175                 180                 185

cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg atc      886
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile
190                 195                 200                 205

acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac tgg      934
Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp Trp
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atc cag gag acg atg aag aac aat tagactggac ccacccacca cagcccatca      988
Ile Gln Glu Thr Met Lys Asn Asn
            225

ccctccattt ccacttggtg tttggttcct gttcactctg ttaataagaa accctaagcc   1048

aagaccctct acgaacattc tttgggcctc ctggactaca ggagatgctg tcacttaata   1108

atcaacctgg ggttcgaaat cagtgagacc tggattcaaa ttctgccttg aaatattgtg   1168

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-35 -30 -25

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
-20 -15 -10

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
-5 -1 1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
15 20 25

Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
30 35 40

Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
45 50 55

Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
60 65 70 75

Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
80 85 90

Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
95 100 105

Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
110 115 120

Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
125 130 135

Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
140 145 150 155

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Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
                160                 165                 170

Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
            175                 180                 185

Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
        190                 195                 200

Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
    205                 210                 215

Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
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cataagctag gagaactgag gcttcaaacc tgaagctatc ta atg agg agg ctg       114
                                              Met Arg Arg Leu
                                                  -45

aag agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc       162
Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg
            -40                 -35                 -30

cct gcc cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct       210
Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala
        -25                 -20                 -15

ctg gta aca ggg cac gta ggg gga gag acg agg atc atc aag ggt tat       258
Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr
    -10                 -5                  -1  1                   5

gag tgc agg cct cac tca cag cca tgg cag gtg gcc ctc ttt cag aag       306
Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys
                10                  15                  20

aca cgg ctt ctc tgt ggg gca acc ctc atc gcc ccc aaa tgg ctc ctg       354
Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu
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                25                  30                  35

aca gca gcc cac tgc cgc aag ccc cat tac gtg atc ctc ctt gga gag      402
Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile Leu Leu Gly Glu
        40                  45                  50

cac aat cta gag aag aca gac ggc tgt gag cag agg cgg atg gcc act      450
His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg Arg Met Ala Thr
    55                  60                  65

gag tcc ttc ccc cac ccc gac ttc aac aac agc ctc ccc aac aaa gac      498
Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu Pro Asn Lys Asp
70                  75                  80                  85

cac cgg aat gac ata atg ctt gtg aag atg tcg tct ccc gtc ttc ttt      546
His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser Pro Val Phe Phe
                90                  95                  100

acc cga gct gtg cag cca ctc acc ctg tcc cca cac tgt gtc gct gca      594
Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His Cys Val Ala Ala
            105                 110                 115

ggc acc agc tgc ctc att tct gga tgg ggc acc acg tcc agc ccc cag      642
Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr Ser Ser Pro Gln
        120                 125                 130

ttg cgc ctg cct cat tcc ttg cga tgt gcc aat gtc tcc atc atc gaa      690
Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val Ser Ile Ile Glu
    135                 140                 145

cac aag gag tgt gag aag gcc tac ccg ggc aac atc aca gac acc atg      738
His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met
150                 155                 160                 165

ctg tgc gcc agt gtt cgg aaa gag ggc aag gac tcc tgt cag ggt gac      786
Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln Gly Asp
                170                 175                 180

tct gga ggc ccc ctg gtc tgc aac gga tct ctt caa ggc atc atc tcc      834
Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile Ser
            185                 190                 195

tgg ggt cag gac cca tgt gcc gtc acc aga aag cct ggt gtc tat aca      882
Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr
        200                 205                 210

aaa gtc tgc aaa tac ttt aac tgg atc cac gag gtt atg agg aac aat      930
Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn
    215                 220                 225

tagaggggac ctgcttccca ccacccaacc cctccaacct cttcttaatg ctttgacttc    990

tcttcattct gccctaagaa gtcctcagct gggaccctgg catgtactct ctccgaccca   1050

ccatgagtat agtataggga tgctctaact tgatgatcga cctggggcct ggaatcaaat   1110

cctgacttga actaaattgt gactctggac atgatcacca ctggttttgt ttgtttggtt   1170

gtttttttgtt ttgttttgtt ttgttcccag ctttgaagac agtccctggc atatcccagg   1230

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-30 -25 -20

Ile Ala Leu Ala Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile
-15 -10 -5 -1 1

Ile Lys Gly Tyr Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala
5 10 15

Leu Phe Gln Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro
20 25 30

Lys Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile
35 40 45

Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg
50 55 60 65

Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu
70 75 80

Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser
85 90 95

Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His
100 105 110

Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr
115 120 125

Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val
130 135 140 145

Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile
150 155 160

Thr Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser
165 170 175

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Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln
        180                 185                 190

Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro
    195                 200                 205

Gly Val Tyr Thr Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val
210                 215                 220                 225

Met Arg Asn Asn


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Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
               -15                 -10                 -5

gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag ccc      152
Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
        -1  1                   5                  10

tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg acg      200
Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr
    15                  20                  25

ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccg      248
Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
30                  35                  40                  45

tgg gtg tca ctc acc tct ccc acc cat gtc tcc ccc gac ctt tcc tcc      296
Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser
                50                  55                  60

tcc aac tac tgt ctc tcc cac ctc agc cgc tac ata gtt cac ctg ggg      344
Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His Leu Gly
            65                  70                  75
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cag cac aac ctc cag aag gag gag ggc tgt gag cag acc cgg aca gcc      392
Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala
        80                  85                  90

act gag tcc ttc ccc cac ccc ggc ttc aac aac agc ctc ccc aac aaa      440
Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
    95                  100                 105

gac cac cgc aat gac atc atg ctg gtg aag atg gca tcg cca gtc tcc      488
Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val Ser
110                 115                 120                 125

atc acc tgg gct gtg cga ccc ctc acc ctc tcc tca cgc tgy gtc act      536
Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys Val Thr
                130                 135                 140

gct ggc acc agc tgc ctc att tcc ggc tgg ggc agc acg tcc agc ccc      584
Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser Ser Pro
            145                 150                 155

cag tta cgc ctg cct cac acc ttg cga tgc gcc aac atc acc atc att      632
Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr Ile Ile
        160                 165                 170

gag cac cag aag tgt gag aac gcc tac ccc ggc aac atc aca gac acc      680
Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr
    175                 180                 185

atg gtg tgt gcc agc gtg cag gaa ggg ggc aag gac tcc tgc cag ggt      728
Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys Gln Gly
190                 195                 200                 205

gac tcc ggg ggc cct ctg gtc tgt aac cag tct ctt caa ggc att atc      776
Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile
                210                 215                 220

tcc tgg ggc cag gat ccg tgt gcg atc acc cga aag cct ggt gtc tac      824
Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr
            225                 230                 235

acg aaa gtc tgc aaa tat gtg gac tgg atc cag gag acg atg aag aac      872
Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met Lys Asn
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Asn

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-5              -1  1                   5                  10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
            15                  20                  25

Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
        30                  35                  40

Lys Pro Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu
    45                  50                  55

Ser Ser Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His
60                  65                  70                  75

Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg
                80                  85                  90

Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro
            95                  100                 105

Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro
        110                 115                 120

Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
    125                 130                 135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser
140                 145                 150                 155

Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr
                160                 165                 170

Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr
            175                 180                 185

Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys
        190                 195                 200

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly
    205                 210                 215

Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly
220                 225                 230                 235

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Lys Asn Asn

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tgctgccccc tttgacgacg atgacaagga tccgaattc 99

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aggatcagga gtagattcat ggtgttgcta gccaagctt 99

<210> 9
<211> 15
<212> DNA
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<220>
<223> Designed oligonucleotide primer to ampify neurosin-encoding seque
nce

<400> 9
ttggtgcatg gcgga 15

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify neurosin-encoding sequ
ence

<400> 10
tcctcgagac ttggcctgaa tggtttt 27

<210> 11
<211> 35
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gcgctagcag atctccatga atctactcct gatcc 35

<210> 12
<211> 29
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<220>
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tgaagcttgc catggaccaa cttgtcatc 29

<210> 13
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<220>
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<400> 13
ccaagcttca ccatcaccat caccat 26

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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<400> 14
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<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify a portion of plasmid p FBTrypSigTag

<400> 15
caaatgtggt atggctg 17

<210> 16
<211> 20

<212> DNA
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<220>
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<400> 16
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<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify active hBSSP6-encoding sequence

<400> 17
cggaattcgc attaagaaga ggttggag 28

<210> 18
<211> 20
<212> DNA
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<400> 18
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<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 19
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<210> 20
<211> 20
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as hBSSP6F3 to amplify full-length human brain BSSP6-encoding mRNA (forward)

<400> 20
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<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6F4 to amplify mature human BSSP6-encoding region (forward)

<400> 21
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<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6F5 to amplify full-length human prostate BSSP6-encoding mRNA (forward)

<400> 22
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<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R1 for RACE f or human BSSP6 (reverse)

<400> 23
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<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R2 for RACE f or human BSSP6 (reverse)

<400> 24
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<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R3/P to ampli fy full-length human BSSP6-encoding mRNA (reverse)

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<210> 26
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<212> DNA
<213> Artificial Sequence

<220>
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or mouse BSSP6 (forward)

<400> 26
cgacttcaac aacagcctcc 20

<210> 27
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<220>
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for mouse BSSP6 (forward)

<400> 27
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<210> 28
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<213> Artificial Sequence

<220>
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<400> 28
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<210> 29
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<220>
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<210> 30
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<220>
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<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6R1 for RACE f
or mouse BSSP6 (reverse)

<400> 31
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<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6R2 for RACE f
or mouse BSSP6 (reverse)

<400> 32
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<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6R3/E to ampli
fy full-length mouse BSSP6-encoding mRNA (reverse)

<400> 33
cggaattcgc attaagaaga ggttggag 28

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R3 to amplify
a portion of BSSP6 variant type-encoding mRNA from human prostat
ic cancer cell line PC-3 (reverse)

<400> 34
atggtgtctg tgatgttgcc 20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP6F7 to amplify a portion of human BSSP6-encoding mRNA (forward)

<400> 35
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<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify conserved region of se rin proteases-encoding sequence

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<223> n is a, c, g or t.

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<223> n is a, c, g or t.

<400> 36
gtgctcacng cngcbcaytg 20

<210> 37
<211> 20
<212> DNA
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<221> misc_feature
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<223> n is a, c, g or t.

<400> 37
ccvctrwsdc cnccnggcga 20

<210> 38
<211> 117
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 38
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tgctgccccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 39
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 39
gaattcggat ccttgtcatc gtcgtcatgg tgatggtgat ggtgaaaggg ggcagcaaca 60

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117

<210> 40
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40

Asp Asp Asp Asp Lys
1 5

<210> 41
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41

Lys Val His Gly
1